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Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
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                                                                                                                                                                                                                                       SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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1877
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

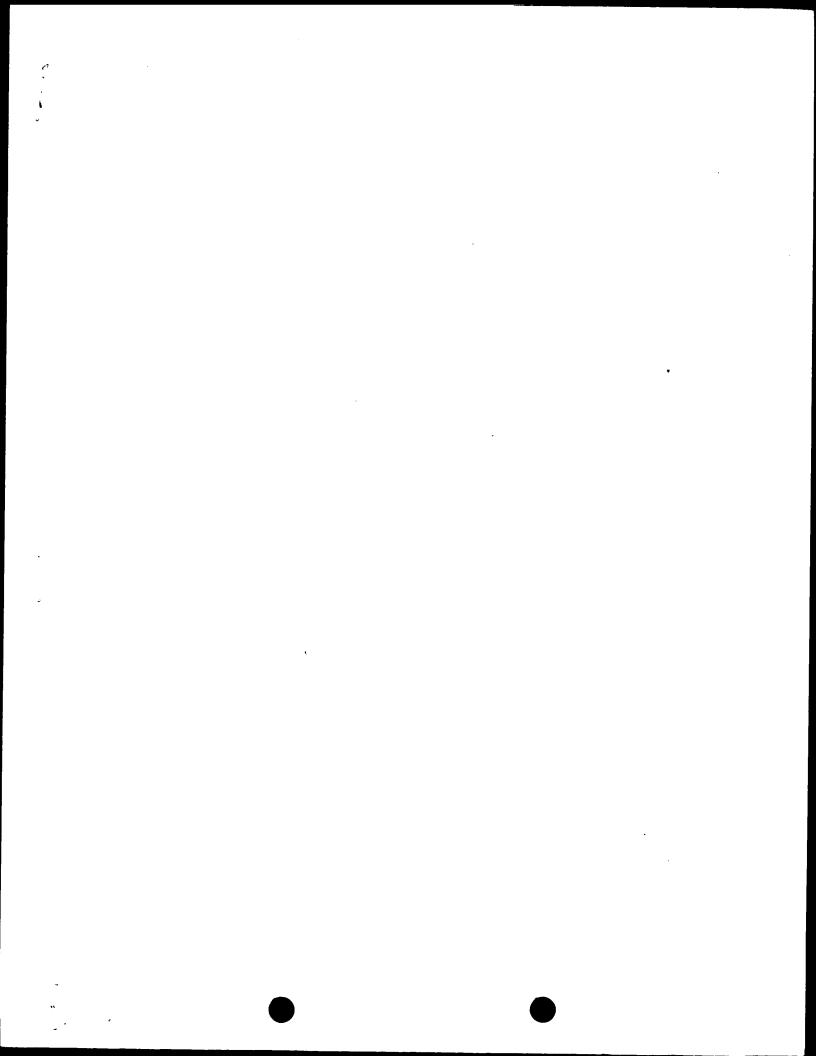
SUMMARIES

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Pfam; Pf03065; Glyco_hydro_57; 1.

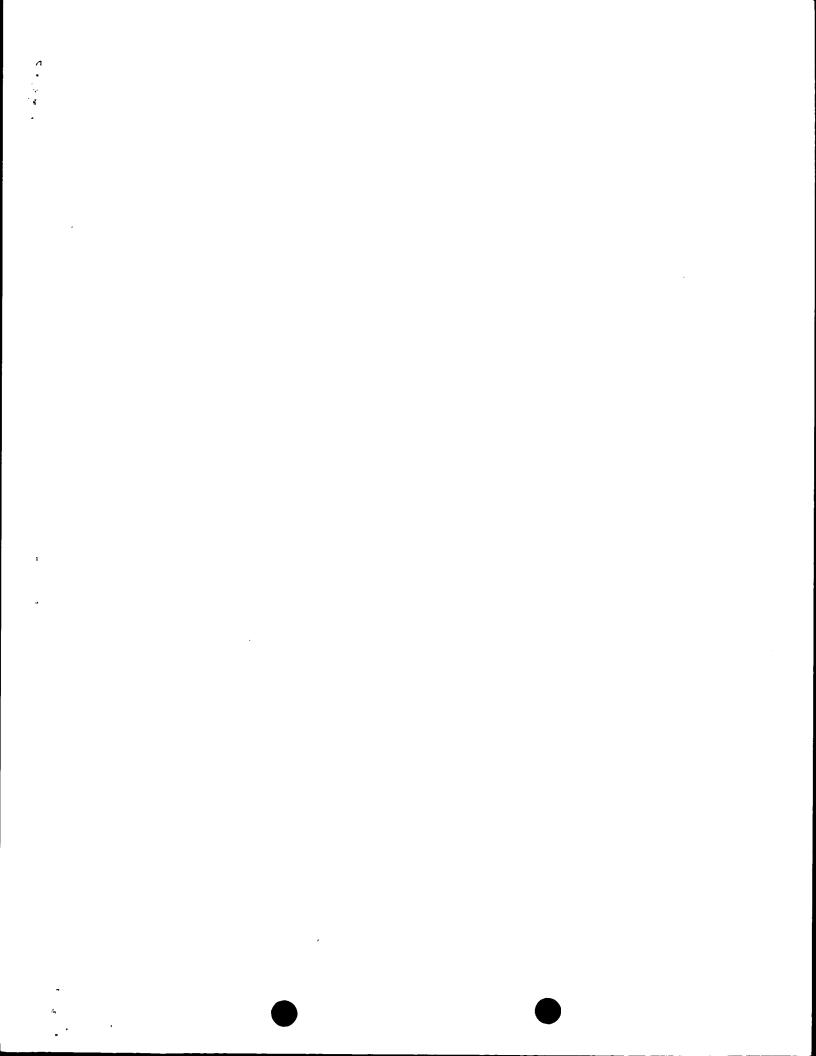
Hypothetical protein; Complete prote
SEQUENCE 364 AA; 41755 MW; 7B4B3
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7B4B36AB4A975BAD CRC64;
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Hypothetical protein; Complete
SEQUENCE 529 AA; 62075 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamu Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T. Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., (Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Cyanobacteria; Chroococcales;
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                           EGPWFIDYLFRKSWFDQDTFEMTHLADYLRGNPHQQVCRPSQSSWGYKGFHEYWLNDTNA
                                                                                 EKAWYD-----PYWAKEKAAEHASNFMYNRQQQVGHLSGIMGRPPLVVSPYDAELFGHWWY
                                                                                                            LKAVKDIEAVPVWVAVNTAV-----WIGI-GRLPLMNPKKVAS-----WI
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Murphy,D. and Reid,J.
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42734. .70133
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70234. .106104
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6723. .10907
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179198. .221284
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106205. .142909
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1.8%; Score 20; DB 6; 100.0%; Pred. No. 16; tive 0; Mismatches
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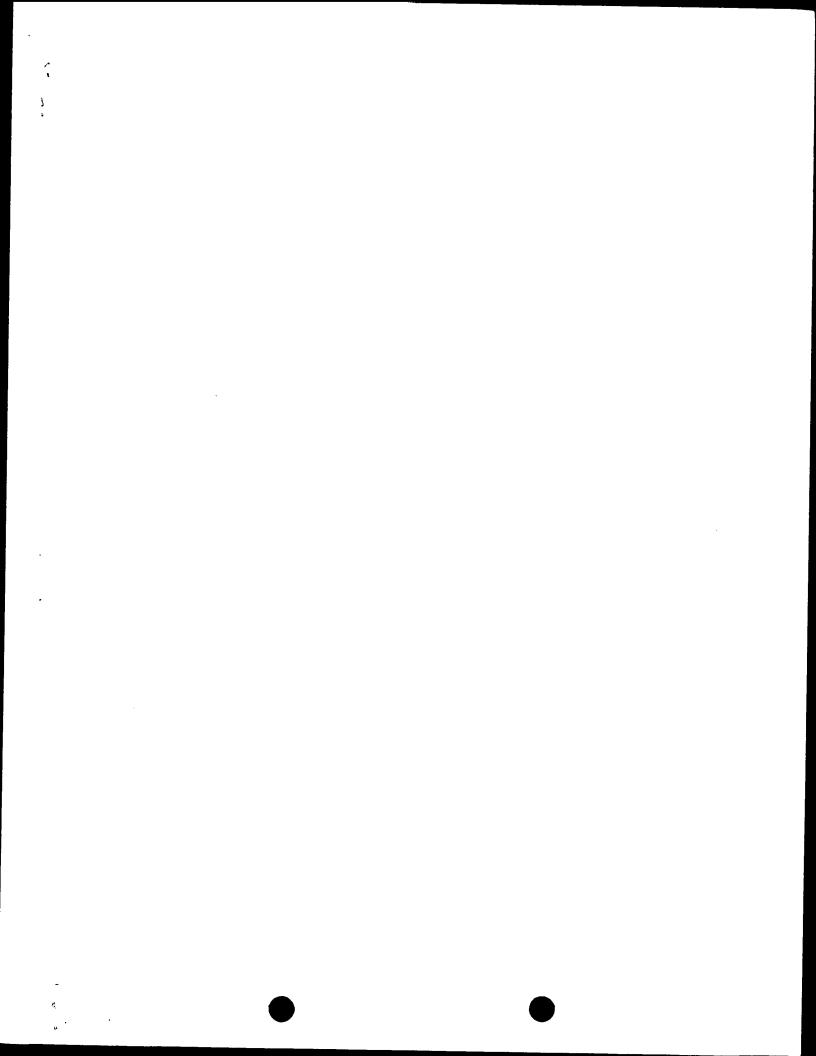
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92046037
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121. .159
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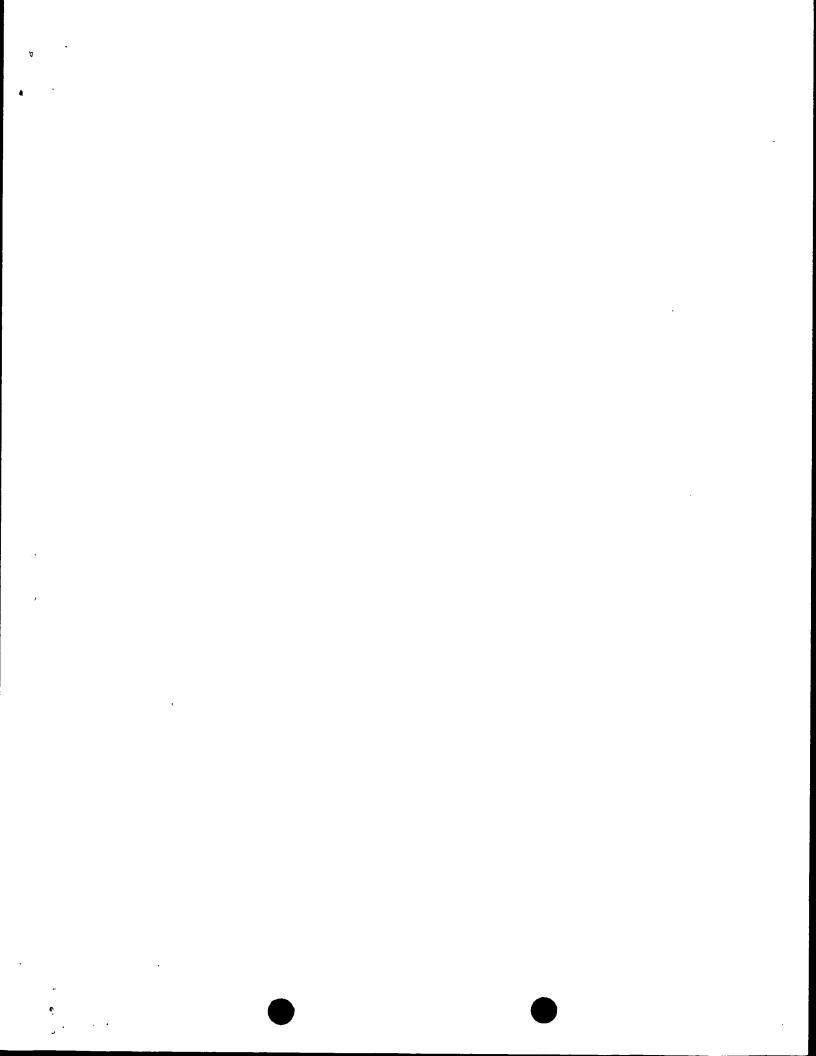
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University and Research Center, Hessel Wageningen NL-6703 CT, The Netherlands
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ELGLPRKIKHSEKKLYLRTSSWAPDKSLRIWTEDEGNARLNMLTSYMDGELAFLAENS
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                                        /note="similar to major facilitator super-family secondary
transport proteins (symport/antiport)"
                                            transport proteins
                                                                               /gene="mfsA"
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CAATTCTCCCACTTCTCCCACTCTCTAGAGTTGAGGCACAAATAAAAAAGAGATAGAGAAG
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SRKYYKSKNECLFCRILKEEKESEERIIYENDNFIVFNFFASWPFEHHIYPKRHVOL
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RIEFIIOHLQYVHKALEDGLDVRGYFYWSFMDNYEWREGFEFRFGLVEVDYETFERRP
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VSYAGPNVRAIVSQVNLPEDRGTVFGLFNILDNVGKAIGPLFGGFLIETLKSMGYMEP
LAYQYTLLIGALFWIPCALVWIWIRKSYPEDRDKVKEILKKRAEEILKSKT"
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ACCESSION DEFINITION Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt. position AP000002

257000 bp

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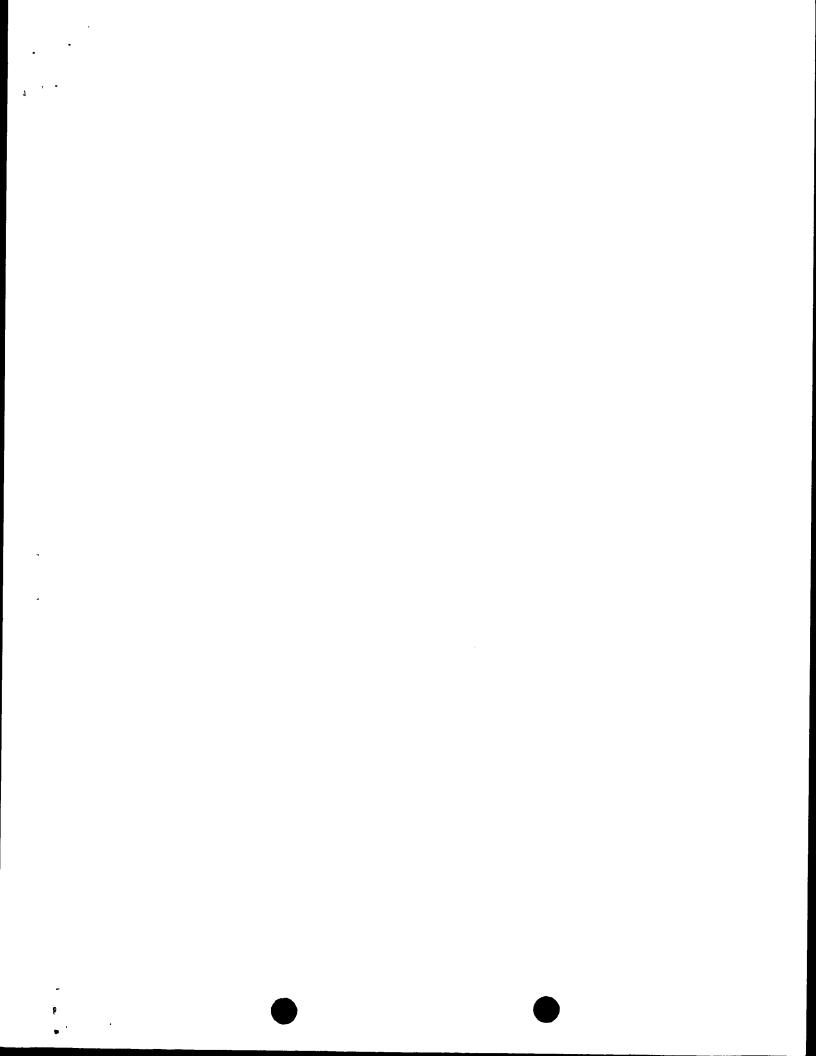
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KEYWORDS VERSION

SOURCE ORGANISM REFERENCE

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AUTHORS AP000002 AB009475 AB009476 AB009477 AB009478 AB009479 AB009480 AB009481 AB009482 AB009483 AB009484 BA000001 AB00902.1 GI:3236129 Kawarabayasi,Y., Sawada,M., Horikawa,H., Yamamoto,S., Sekine,M., Baba,S., Kosugi, Pyrococcus horikoshii (strain:OT3) DNA Pyrococcus horikoshii Thermococcaceae; Pyrococcus Archaea; Euryarchaeota; Thermococci; Thermococcales; (sites) Kosugi, H., Hosoyama, A., Nagai, Y., Haikawa,Y., Hino,Y.,



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On Jul 28, 1998 this sequence version replaced gi:3130553 gi:3130577 gi:3130627 gi:3130656 gi:3130685 gi:3130705 gi:3130737 gi:3130785 gi:3130828 gi:3130828.
AB009475-AB009484: submitted (10-DEC-1997)
Kawarabayasi, Y. is officially affiliated with the National
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Restriction map, ORF organization, sequence alignment and more information are available at W.W.W. site of Biotechnology Center, URL: http://www.bio.nite.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenPept release 103; EMBL release 52.0; SwissProt release 34.0; PIR-Protein release 54.0; and OWL release 29.5. E-mail address for comments and questions: genomeOT3@nite.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maryland, Baltimore, MD, USA.
Horikoshi, K. is at the Japan Marine Science and Technology Center,
Yokosuka, Kanagawa 237-0061, Japan.
Masuchi, Y. is at the University of Tokyo, Meguro, Tokyo 153-0041,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka, T., Kawarabayasi, Y. and Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
All the sequence with length 100 codons or more between ATG or GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shizuya, H. is at the California Institute of Technology, Pasadena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305-0046,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The other authors are at the National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute of Bioscience and Human-Technology, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 257000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stop codon are defined as CDS
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complement(1645. .1974)
                          complement(1645. .1974)
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                                                                                                                                                                                                                                                    KDGYFVVPNARATWIAMHRERLRETLVKEAKVPTSRYMYATTLDELYEACEKIGYPCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="287001-544000 nt. position"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain-"OT3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism-"Pyrococcus horikoshii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is at the Center of Marine Biotechnology, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               РН0318"
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FEATURES

CDS

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/product="177aa long hypothetical
phosphoribosylaminoimidazole carboxylase catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to ow1:SSOUREK percent identity: 68.000 in 150aa; PIR:S76001 percent identity: 60.694 in 173aa; ow1:BAPURKE1 percent identity: 62.329 in 146aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3275. .4036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAMITDLFTGLIEFIKGCSVHIPGSRNLCFLHKGFPKPLPVHSYPGSSCIWNYKITIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="219aa long hypothetical protein"
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DDVVFVSKLKEWAIKTLKTTNIANFWFFTYLSSGICKLFSNPLLTYKLIWALREEIL
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RYLETSAEVRYGHPAYKKYPRGTNFWLWEGVYDKRVLLSVYRRADYVLKTRSSLGENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3275. .4036)
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/product="438aa long hypothetical
phosphoribosylamide--glycine ligase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4856. .6172
/gene="PH0323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4039. .4698)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PH0321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDSLLSIVOMPSGIPVATVAIDNAKNAALLALRILGIKYPEIKEKLRRYMKDMKRKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=
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                                                                                                                                                                                                                                                                                                                                                            motif-prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYRPKTIITYSQLECPILEETVYLASDIVLETRIINGKKVGIITKGPNENLIFELFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="PH0322"
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NKAWAREFMERNNIPGRKMFRIFDDVQEMRKWIDEYGKPVVVKPLGLTGGKGVKVVGY
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/transl_table=11
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Matches
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                                                                                                                                                                                                  45405 CAATTCTTCCACTCCTCACCCTCTCCAGGATTGAGGCCCCAAATAAAACGTGATAGAGAGA 45346
                                                                                                                                                                                                                                                                                                     45465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45585
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                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tgagagcgctcgtctttcacggcaacctccagtatgccgaaatcccaaagagcgaaatcc 61
                                                                                                                                                                                                                                                                                                                                                                                                                           cttttgggctcaacataacgggctataccttáaagttcctcccgaaggatattatagacc 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    caaaggtcatagagaaggcatacatcccagtcatcgagacactgattaaagaagaaattc 121
                                                                                                                                                                                                                                                                                                                                                                                                      CTTTCGGCCTAAACATAACCGGTTATTCACTGCAATTTCTCCCCCAGGAATTAATCCACC 45466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAAGGTTATAGAAAAATCCTACTTTCCAACTATTTCGGAGCTTATAAAAAGGGAGATAC 45526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGAGCATTGATCTTCCATGGAAATTTGCAATACGCCGAAATACCAAAGCATGAAATCT 45586
                          acccgataatccctgccatactgaaggacaacggttatgagtatctattcgccgacgggg 421
                                                                                                                        ttaaggaagagctcttcgagctttctccaaagggattctggctgccagagctcgcctatg 361
                                                                                                                                                                                                                                                                                                     TCATTAAAGAAGGAATCGAAAGTGAACTTATAGAAATTCTTGGAACAAGTTATACTCACG
                                                                                                                                                                                                                                                                                                                                ATCCGATAATTCCAGCAATTTTAAGAGACAATGAATACGAATATCTCTTTGCCGACGGAG
                                                                                                                                                                                                                                              caatactccccctcctcccgcttagcagagtagaagcacaagttcagagagatagggaag 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               748; Conservative
                                                                                                 TAAAGGAAGAGATATTCGAGGTTTCTCCTGGAGGATTTTGGCTTCCCGAGTTGGCCTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDVGPITGGMGSYSCSNHLLPFITEGDFERALKTLEETIEAMRKEGYPYKGILYGQFM
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6174. .7325
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CGHASATLRESLLEKVFDMAEKYVEATKKYYPPGIIGPFTLQTVVDKDLNFYIFDVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PH0324"
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YFKFFGEFSDEITEEEFEGLRGIIIDELEHEKFFSESKKLFVENIRDFVLGMNDGLV
BILGAVTGLSAVYPNSPRLVGISGLLVGVAGALSMGIGALISVRSQROVSEAIRERTK
ILFKVSPEKAKEELYEKLVEGGLPEEIAREVSEKLLEKEEAIIKLLVEEEEENEFRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEMVTTGLGAAFLSYIFGHIMESLFNVSAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYTGIAYLFGVAFPVTPYFFASTSLRALPISVTLAGLALAIVATSISLISGISIRKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 540.4; DB 1;
pred. No. 1.9e-149;
0; Mismatches 346;
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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